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	Patents ADP number *(if you know it)*	53193901mb
	If the applicant is a corporate body, give the country/state of its incorporation	BELGIUM
4.	Title of the invention	NEUROTROPHIC FACTOR RECEPTOR
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NEUROTROPHIC FACTOR RECEPTOR

The present invention is concerned with cloning and expression of a novel human receptor protein, designated herein GRFα5 and in particular with an isolated nucleic acid sequence encoding the GFRα5 protein, an expression vector comprising said nucleic acid sequence, a host cell transformed or transfected with said vector, isolated GRFα5 protein, compounds which act as agonists or antagonists in relation to GFRα5 and methods of identifying them, together with pharmaceutical compositions comprising the isolated nucleic acid, the receptor protein or said agonist or antagonist.

Neurotrophic growth factors are involved in neuronal differentiation, development and maintenance. These proteins can prevent degeneration and promote survival of different types of neuronal cells and are thus potential therapeutic agents for neurodegenerative diseases. Glial cell-line derived neurotrophic factor (GDNF) was the first member of a growing subfamily of neurotrophic factors structurally distinct from the neurotrophins. GDNF is a distantly related member of the transforming growth factor β (TGF-β) superfamily of growth factors, characterized by a specific pattern of seven highly conserved cysteine residues within the amino acid sequence (Kingsley, 1994). GDNF was originally purified using an assay based on its ability to maintain the survival and function of embryonic ventral midbrain dopaminergic neurons *in vitro* (Lin et al., 1993). Other neuronal cell types in the central (CNS) or peripheral nervous systems (PNS) have been shown to be responsive to the survival effects of GDNF (Henderson et al., 1994, Buj-Bello et

al., 1995, Mount et al., 1995, Oppenheim et al., 1995). GDNF is produced by cells in an inactive proform, which is cleaved specifically at a RXXR recognition site to produce active GDNF (Lin et al., 1993). In view of its effects on dopaminergic neurons, clinical trials have evaluated GDNF as a possible treatment for Parkinson's disease, a common neurodegenerative disorder characterized by the loss of a high percentage (up to 70 %) of dopaminergic cells in the substantia nigra of the brain. Exogenous administration of GDNF has potent protective effects in animal models of Parkinson's disease (Henderson et al., 1994, Beck et al., 1995, Tomac et al., 1995, Yan et al., 1995, Gash et al., 1996, Choi-Lundberg et al., 1997, Bilang-Bleuel et al., 1997, Mandel et al., 1997).

Recently, three new members of the GDNF family of neurotrophic factors have been discovered. Neurturin (NTN) was purified from conditioned medium from Chinese hamster ovary (CHO) cells using an assay based on the ability to promote the survival of sympathetic neurons in culture (Kotzbauer et al., 1996). The mature neurturin protein is 57% similar to mature GDNF. Persephin (PSP) was discovered by degenerate primer PCR using genomic DNA. The mature protein, like mature GDNF, promotes the survival of ventral midbrain dopaminergic neurons and of motor neurons in culture (Milbrandt et al., 1998). The similarity of the mature persephin protein with mature GDNF and neurturin is ≈ 50 %. Very recently, a fourth member has been cloned using genomic DNA information in the public EMBL database and has been named Enovin (EVN) (Masure et al., 1999) or Artemin (ARTN) (Baloh et al., 1998b). This factor is ± 57 % similar to NTN and PSP and acts

primarily on peripheral neurons.

All four GDNF family members require a heterodimeric receptor complex in order to carry out downstream intracellular signal transduction. GDNF binds to the GDNF family receptor alpha 1 (GFRα-1; also termed GDNFRα, RETL1 or TrnR1; GFRα Nomenclature Committee, 1997) subunit, a glycosyl phosphatidyl inositol (GPI)-anchored membrane protein (Jing et al., 1996, Treanor et al., 1996, Sanicola et al., 1997). The GDNF/GFRα-1 complex subsequently binds to and activates the cRET proto-oncogene, a membrane bound tyrosine kinase (Durbec et al., 1996, Trupp et al., 1996), resulting in phosphorylation of tyrosine residues in cRET and subsequent activation of downstream signal transduction pathways (Worby et al., 1996). GFRα-2 (also termed RETL2, NTNR-α, GDNFR-β or TrnR2), which is similar to GFRα-1, has been identified by a number of different groups (Baloh et al., 1997, Sanicola et al., 1997, Klein et al., 1997, Buj-Bello et al., 1997, Suvanto et al., 1997). The human GFRα-1 and GFRα-2 receptor subunits are 49% identical and 63% similar by protein sequence with 30 of the 31 cysteine residues conserved. Both receptors contain a hydrophobic domain at their carboxy-termini involved in GPI anchoring to the membrane. GFRα-1 and GFRα-2 are widely expressed in almost all tissues and expression may be developmentally regulated (Sanicola et al., 1997, Widenfalk et al., 1997).

GFRα-1 is the preferred receptor for GDNF, whereas GFRα-2 preferentially binds neurturin (Jing et al., 1996, Treanor et al., 1996, Klein et al., 1997). It is also clear, however, that there is some cross-talk between these growth factors and receptors as GDNF can

bind to GFRα-2 in the presence of cRET (Sanicola et al., 1997) and neurturin can bind to GFRα-1 with low affinity (Klein et al., 1997). GDNF and neurturin are thus part of a neurotrophic signalling system whereby different ligand-binding subunits (GFRα-1 and GFRα-2) can interact with the same tyrosine kinase subunit (cRET).

Recently, a third member of the GFRα family of coreceptors, GFRα-3, has been described (Jing et al., 1997, Masure et al., 1998, Worby et al., 1998, Naveilhan et al., 1998, Baloh et al., 1998a). This receptor's amino acid sequence is 35% identical to both GFRα-1 and GFRα-2. GFRα-3 is not expressed in the developing or adult CNS, but is highly expressed in several developing and adult sensory and sympathetic ganglia of the PNS (Widenfalk et al., 1998, Naveilhan et al., 1998, Baloh et al., 1998a). GFRα-3 has been shown to be the preferred coreceptor for Enovin/artemin and also signals via cRET (Masure et al., 1999, Baloh et al., 1998b). Crosstalk between EVN/ARTN and GFRα-1 seems also possible, at least *in vitro*.

A fourth member of the GFRα family has been identified in chicken (Thompson et al., 1998) and has been shown to mediate signalling of persephin via cRET (Enokido et al., 1998). A functional mammalian homologue encoding a mammalian persephin receptor has yet to be discovered.

The present inventors have surprisingly identified a further novel human receptor of the GDNF family designated herein as GFRα-5. The DNA sequence has been cloned and a number of splice variants encoding

the receptor have also been identified.

Accordingly, there is provided by the present invention a nucleic acid encoding a receptor protein designated GFRα-5 having the amino acid sequence illustrated in Sequence ID No's. 8 or 9 or encoding a functional equivalent, derivative or bioprecursor of said receptor.

Advantageously, the nucleic acid molecule according to the invention may be used for expression of said GFRα-5 protein in, for example, a host cell or the like, using an appropriate expression vector. Preferably, the nucleic acid molecule is a DNA molecule, and even more preferably a cDNA molecule having a sequence as illustrated in any of Sequence ID No's. 5 to 7 or the complement thereof. Alternatively, the nucleic acid molecule is capable of hybridising to the sequences of the invention under conditions of high stringency or to the complement thereof. Stringency of hybridisation as used herein refers to conditions under which polynucleic acids are stable. The stability of hybrids is reflected in the melting temperature (Tm) of the hybrids. Tm can be approximated by the formula:

$$81.5°C+16.6(1og_{10}[Na^+]+0.41\ (\%G\&C)-6001/1$$

wherein 1 is the length of the hybrids in nucleotides. Tm decreases approximately by 1-1.5°C with every 1% decrease in sequence homology.

The nucleic acid capable of hybridising to nucleic acid molecules according to the invention will generally be at least 70%, preferably at least 80 or

90% and more preferably at least 95% homologous to the nucleotide sequences according to the invention.

Advantageously, the antisense molecule may be used as a probe or as a medicament or in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient.

According to a second aspect of the invention, there is provided a DNA expression vector comprising the DNA molecule according to the invention. This vector may, advantageously, be used to transform or transfect a host cell to achieve expression of GFRα-5 according to the invention. Preferably, the DNA is included in a plasmid, for subsequent transfection or transformation of the host cell.

An expression vector according to the invention includes a vector having a nucleic acid according to the invention operably linked to regulatory sequences, such as promoter regions, that are capable of effecting expression of said DNA fragments. The term "operably linked" refers to a juxta position wherein the components described are in a relationship permitting them to function in their intended manner. Such vectors may be transformed into a suitable host cell to provide for expression of a polypeptide according to the invention. Thus, in a further aspect, the invention provides a process for preparing receptors according to the invention which comprises cultivating a host cell, transformed or transfected with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the receptors, and recovering the expressed receptors.

The vectors may be, for example, plasmid, virus or phage vectors provided with an origin of replication, optionally a promoter for the expression of said nucleotide and optionally a regulator of the promoter. The vectors may contain one or more selectable markers, such as, for example, ampicillin resistance.

Regulatory elements required for expression include promoter sequences to bind RNA polymerase and transcription initiation sequences for ribosome binding. For example, a bacterial expression vector may include a promoter such as the lac promoter and for transcription initiation in the Shine-Dalgarno sequence and the start codon AUG. Similarly, a eukaryotic expression vector may include a heterologous or homologous promoter for RNA polymerase II, a downstream polyadenylation signal, the start codon AUG, and a termination codon for detachment of the ribosome. Such vectors may be obtained commercially or assembled from the sequences described by methods well known in the art.

Nucleic acid molecules according to the invention may be inserted into the vectors described in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may be produced by synthetic means.

In accordance with the present invention, a defined nucleic acid includes not only the identical nucleic acid but also any amino base variations including, in particular, substitutions in bases which result in a synonymous codon (a different codon specifying the same amino acid residue) due to the degenerate code in conservative amino acid substitutions. The term

"nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given regarding base variations.

The present invention also advantageously provides nucleic acid sequences of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously, be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as, by recombinant or synthetic means. They may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting for the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesised *in situ* on the array. (See Lockhart *et al.*, Nature Biotechnology, vol. 14, December 1996 "Expression monitoring by hybridisation into high density oligonucleotide arrays". A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations.

The nucleic acid sequences, according to the invention may be produced using such recombinant or synthetic

means, such as, for example, using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from a human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al* (Molecular Cloning: a Laboratory Manual, 1989).

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P or ^{35}S, enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using known techniques *per se*.

The present invention also comprises within its scope proteins or polypeptides encoded by the nucleic acid molecules according to the invention or a functional equivalent, derivative or bioprecursor thereof. Preferably, the protein comprises the amino acid sequence of Sequence ID No's. 8 and 9.

A "functional equivalent" as defined herein should be taken to mean a receptor that exhibits the same properties and functionality associated with the GFRα-5 receptor according to the invention. A "derivative" should be taken to mean a polypeptide or protein in which certain amino acids may have been

altered or deleted or replaced and which polypeptide or protein retains biological activity of said GFRα-5 receptor and/or which can cross react with antibodies raised using a receptor according to the invention as the challenging antigen.

Encompassed with the scope of the invention are hybrid and modified forms of the GFRα-5 receptor according to the invention including fusion proteins and fragments. The hybrid and modified forms include, for example, when certain amino acids have been subjected to some modification or replacement, such as for example, by point mutation and yet which results in a protein which possesses the same receptor specificity as the GFRα-5 receptor of the invention.

The protein according to the invention should be taken to include all possible amino acid variants encoded by the nucleic acid molecule according to the invention including a polypeptide encoded by said molecule and having conservative amino acid changes. Proteins or polypeptides according to the invention further include variants of such sequences, including naturally occurring allelic variants which are substantially homologous to said proteins or polypeptides. In this context, substantial homology is regarded as a sequence which has at least 70%, and preferably 80 or 90% amino acid homology with the proteins or polypeptides encoded by the nucleic acid molecules according to the invention.

A further aspect of the invention comprises the host cell itself transformed with the DNA expression vector described herein, which host cell preferably comprises a eukaryotic cell, which may be for example, a

mammalian cell, an insect cell or yeast cell or the like. In one embodiment the cell comprises a human embryonic kidney cell and preferably a cell of the HEK293 cell line. Alternatively, the cell may comprise NIH/373 mouse fibroblasts or Chinese hamster ovary (CHO) cells or COS-7 cells.

Further provided by the present invention is a transgenic cell, tissue or organism comprising a transgene capable of expressing GFRα-5 according to the invention, or of expressing a functional equivalent, derivative or bioprecusor of said receptor. The term "transgene capable of expression" as used herein means a suitable nucleic acid sequence which leads to expression of a human receptor having the same function and/or activity as GFRα-5. The transgene may include, for example, genomic nucleic acid isolated from rat cells or synthetic nucleic acid, including cDNA, integrated into the genome or in an extra chromosomal state. Preferably, the transgene comprises the nucleic acid sequence encoding GFRα-5 according to the invention or a functional fragment of said nucleic acid. A functional fragment of said nucleic acid should be taken to mean a fragment of the gene or cDNA encoding GFRα-5 receptor or a functional equivalent or bioprecursor of said GFRα-5 which fragment is capable of being expressed to produce a functional receptor protein. For example, the gene may comprise deletions of mutations but may still encode a functional receptor.

Further provided by the present invention is an isolated or purified GFRα-5 protein having the amino acid sequence illustrated in Sequence ID No's. 8 or 9 or a functional fragment or bioprecursor of said

receptor or alternatively a GFRα-5 protein expressed by the transgenic cell, tissue or organism according to the invention. Also provided by the invention are membrane preparations from cells expressing GFRα-5.

The present invention is further directed to inhibiting GFRα-5 *in vivo* by the use of antisense technology. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the mature protein sequence, which encodes for the protein of the present invention, is used to design an antisense RNA oligonucleotide of from 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple-helix - see Lee *et al.* Nucl. Acids Res., 6:3073 (1979); Cooney *et al.*, Science, 241:456 (1988); and Dervan *et al.*, Science, 251: 1360 (1991), thereby preventing transcription and the production of GFRα-5. The antisense RNA oligonucleotide hybridises to the mRNA *in vivo* and blocks translation of an mRNA molecule into the GFRα-5 receptor.

Antibodies to the GFRα-5 receptor according to the invention are also provided which may be used in a medicament or in a pharmaceutical composition.

Antibodies to the GFRα-5 of the invention may, advantageously, be prepared by techniques which are known in the art. For example, polyclonal antibodies may be prepared by inoculating a host animal, such as a mouse, with the polypeptide according to the invention or an epitope thereof and recovering immune

serum. Monoclonal antibodies may be prepared according to known techniques such as described by Kohler R. and Milstein C., Nature (1975) 256, 495-497.

Antibodies according to the invention may also be used in a method of detecting for the presence of GFRα-5 by reacting the antibody with a sample and identifying any protein bound thereto. A kit may also be provided for performing said method which comprises an antibody according to the invention and means for reacting the antibody with said sample.

Advantageously, the antibody according to the invention may also be used as a medicament or in the preparation of a medicament for treating diseases associated with expression of the GFRα-5 of the invention. The invention also further provides a pharmaceutical composition comprising said antibody together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all

of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as, a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

Proteins which bind to the GFRα-5 receptor can be identified using this technique. The proteins identified can also be used to identify compounds which acts as agonists/antagonists of these proteins. The structure of the receptor can also be used to design agonists or antagonists of the receptor. The present invention also comprises an agonist or antagonist of the human GFRα-5 receptor according to the invention which agonist or antagonist advantageously may also be used as a medicament or in a pharmaceutical composition together with a pharmaceutically acceptable carrier diluent or excipient therefor.

Agonists or antagonists may be identified by contacting a cell expressing GFRα-5 with a compound to be tested and monitoring the degree of any GFRα-5 mediated functional or biological response, such as for example, by monitoring the level of phosphorylation in said cell or by cytosensor or ligand binding assays in the presence of cRET or

similar proteins in the signal transduction pathway. Preferably, the cell may be a host cell or transgenic cell according to the invention as defined herein. Agonists and antagonists of GFRα-5 may also be identified by, for example, contacting a membrane preparation comprising GFRα-5 with the compound to be tested in the presence of cRET or other similar proteins involved in the signal transduction pathway of which GFRα-5 is a component and monitoring the interaction of GFRα-5 with cRET or said similar proteins. Advantageously, any compounds or molecules identified as agonists or antagonists in relation to GFRα-5 may themselves be used in a pharmaceutical composition as defined above or as a medicament.

Also provided by the invention are molecules or compounds that act on the signal transduction pathway of which GFRα-5 or a functional equivalent belong or alternatively which interfere with complex formation or interaction of GFRα-5 or its functional equivalent, with cRET or a similar protein in the signal transduction pathway of which GFRα-5 is a component.

Compounds identified as agonists or antagonists in relation to GFRα-5 or as ligands or compounds which interfere with the signal transduction pathway of which GFRα-5 is a part, may advantageously be used in the preparation of a medicament for treatment of neurodegenerative diseases, such as, for example, Alzheimers disease, Parkinsons disease, Motor Neuron Disease, peripheral neuropathy, spinal cord injury, familial hirschsprung disease, in addition to various carcinomas such as for example in gastrointestinal cancer and also in treatment of diseases which may be associated with GFRα-5 dysfunction. Compounds

identified as antagonists may, advantageously, be used in the preparation of a medicament for the treatment of carcinoma or in alleviating pain.

The present invention also further comprises a method of identifying ligands of GFRα-5 according to the invention, which method comprises contacting said receptor with either a cell extract or alternatively a compound to be tested for its potential as a GFRα-5 ligand, and isolating any molecules bound to GFRα-5.

A diagnostic kit is also provided by the present invention, which kit, comprises a probe including any of, a nucleic acid molecule encoding a GFRα-5 protein according to the invention, a molecule capable of hybridising thereto under high stringency conditions, a fragment of said nucleic acids, an antisense molecule according to the invention, together with means for contacting biological material to be tested with said nucleic acid probe. A diagnostic kit in accordance with the invention may also comprise an agonist or antagonist in relation to GFRα-5 or an antibody, preferably a monoclonal antibody to GFRα-5. Thus, advantageously, the kit may be used, as appropriate to identify, for example, cells expressing or lacking in said receptor or genetic defects or the like or for determining whether a compound is a agonist or an antagonist of GFRα-5 receptor. Kits for determining whether a compound is an agonist or an antagonist in relation to GFRα-5 may comprise a cell or membrane preparation expressing said receptor according to the present invention, means for contacting said cell with said compound and means for monitoring the level of any GFRα-5 mediated functional or biological response, by for example measuring the

level of phosphorylation in said cell or by cytosensor or ligand binding assays in the presence of cRET or similar proteins involved in the signal transduction pathway of which GFRα-5 is a component.

The present invention may be more clearly understood from the following exemplary embodiment with reference to the accompanying figures wherein;

Figure 1: is an illustration of the Structure of the rat GFRα-5 gene. The top line shows a scale in bp. The line below shows the genomic structure of the rat GFRα-5 gene. Exons are represented by boxes and numbered, intron sequences are depicted as lines. The sizes (in bp) of introns and exons are indicated above the diagram. The translation start codon is indicated by an arrow and the stop codon by an asterisk. The cDNA sequences of variants A and B obtained by splicing out the intron sequences is shown below the genomic sequence. *Alternative splicing of intron 5 results in an earlier stop codon in splice variant B.* The predicted protein sequences of variants A and B are shown at the bottom. The predicted signal peptide, a putative N-glycosylation site and a hydrophobic COOH-terminal region preceded by one or two possible sites for GPI-cleavage *(in variant A only)* are indicated on the diagrams.

Figure 2: is an alignment of the predicted protein sequences of splice variants A and B of rat GFRα-5. The sequences of rat GFRα-5 splice variants A and B were aligned using the ClustalW alignment program (EMBL, Heidelberg, Germany). Amino acid residues conserved between the 2 variants are included in the black areas. Amino acid residues are numbered to the

right. The dashes indicate gaps introduced into the sequence to optimize the alignment.

Figure 3: is an alignment of the predicted protein sequences of GFRα family members. The sequence of rat GFRα-5 variants A and B, rat GFRα-1 (EMBL acc. no. U59486), rat GFRα-2 (EMBL acc. no. AF003825), mouse GFRα-3 (EMBL acc. no. AB008833) and chicken GFRα-4 (EMBL acc. no. AF045162) were aligned using the ClustalW alignment program (EMBL, Heidelberg, Germany). Amino acid residues conserved between all 6 proteins are included in the black areas. Residues conserved between 4 or 5 of the sequences are shaded in grey. Cysteine residues conserved between all six GFRα's are indicated with an asterisk above the sequence. Amino acid residues are numbered to the right. The dashes indicate gaps introduced into the sequence to optimize the alignment.

Oligonucleotide synthesis for PCR and DNA sequencing.

All oligonucleotide primers used were ordered from Eurogentec (Seraing, Belgium). Insert-specific sequencing primers (15- and 16-mers) and primers for use in PCR reactions were designed manually. DNA was prepared on Qiagen-tip-20 or -100 anion exchange or Qiaquick spin columns (Qiagen GmbH, Düsseldorf, Germany) and recovered from the columns in 30 μl TE-buffer (10 mM Tris.HCl, 1 mM EDTA (sodium salt), pH 8.0). Sequencing reactions were done on both strands using the ABI prism BigDye Terminator Cycle sequencing kit and were run on an Applied Biosystems 377XL sequencer (Perkin Elmer, ABI Division, Foster City, CA, USA). The Sequencher™ software was used for sequence assembly and manual editing (GeneCodes,

AnnArbor, MI, USA).

Identification of a cDNA sequence encoding a novel member of the GFRα family

Using the human GFRα-1, GFRα-2 or GFRα-3 DNA or protein sequences as the query sequence, BLAST (Basic Local Alignment Search Tool; Altschul et al., 1990) searches were performed on the daily updates of the public EMBL database. A mouse EST (expressed sequence tag) sequence with EMBL accession number AU035938 showed homology to GFRα-1, GFRα-2 and GFRα-3. The smallest sum probabilities (SSP) obtained by the BLAST analyses are summarized in Table 1.

Table 1: BLAST results.

Query sequence	DNA/PROTEIN	SSP
GFRα-1	protein	7.5e-25
GFRα-2	protein	1.3e-12
GFRα-3	protein	2.2e-20
GFRα-1	DNA	6.6e-09
GFRα-2	DNA	>0.011
GFRα-3	DNA	0.0096

AU035938 (sequence 1) is a sequence of 792 bp derived from a mouse brain cDNA library. To obtain consistent homology with other members of the GFRα family upon translation a frame shift has to be introduced near position 165 in the DNA sequence. It is not clear whether this is due to a sequencing error or whether there is another explanation. Using this EST sequence as the query sequence, the BLAST search against the public EMBL database was repeated. One additional clone (acc. no. AA823200; sequence 2) yielded a significant SSP of 1e-18. Upon inspection of this 497 bp clone, which was derived from a mouse mammary gland cDNA library, only the first 61 bp were identical with

part of AU035938 (position 353 to 415). The rest of the sequence of AA823200 was different from AU035938, but contained parts of which the translated amino acid sequence showed homology with the other GFRα's. Therefore it was hypothesized that AU035938 and AA823200 could represent two variant forms of the same receptor, which was called GFRα-5.

Cloning of mouse GFRα-5 cDNA

First, we tried to amplify a fragment of the mouse GFRα-5 cDNA on Marathon Ready™ cDNAs (Clontech Laboratories, Palo Alto, CA, USA) derived from mouse brain and mouse embryo. Primers were designed using the EST sequences (EMBL acc. no. AU035938 and AA823200) to amplify a 274 bp fragment of mouse GFRα-5. The primers used for the amplification of mouse GFRα-5 are shown in the table below.

Table 2: Primers used for the amplification of mouse GFRα-5 DNA sequences.

Name	Sequence	n
MOUSE-GFRα5-sp2	CGCGTTGTCTGCGCGTCTACG	21
MOUSE-GFRα5-sp3	CGGCGCGAAGAATGCGAAGC	20
MOUSE-GFRα5-ap2	CACCCACGTACCATGGCATGTGC	23

PCR reactions were done using the Taq polymerase system (Boehringer Mannheim, Mannheim, Germany). PCR reactions were performed in a total volume of 50 µl, containing 1x Taq PCR reaction buffer, 0.25 mM dNTP, 0.5 µM of primers MOUSE-GFRα5-sp2 and MOUSE-GFRα5-ap2, 1 µl of Taq polymerase and 2 µl of mouse embryo or mouse brain Marathon Ready™ cDNA. Samples were heated to 95°C for 5 min and cycling was done for 30 s at

94°C, 1 min at 60°C and 45 s at 72°C for 35 cycles, with a final step of 7 min at 72°C. A semi-nested PCR was then performed on 1 µl of the primary PCR reaction with primers MOUSE-GFRα5-sp3 and MOUSE-GFRα5-ap2. PCR reactions were performed in a total volume of 50 µl, containing 1x Taq PCR reaction buffer, 0.25 mM dNTP, 0.5 µM of primers MOUSE-GFRα5-sp3 and MOUSE-GFRα5-ap2, 1 µl of Taq polymerase and 1 µl of primary PCR product. Samples were heated to 95°C for 5 min and cycling was done for 30 s at 94°C, 1 min at 60°C and 45 s at 72°C for 35 cycles, with a final step of 7 min at 72°C. PCR products were analysed on a 1% (w/v) agarose gel in 1x TAE buffer (40 mM Tris-acetate, 1 mM EDTA (sodium salt), pH 8.3). A PCR fragment of the expected size (270 bp) was excised from the gel and purified with the Qiaquick gel extraction kit (Qiagen Gmbh, Hilden, Germany). The PCR fragments were sequenced to confirm their identity. The obtained sequence corresponded to the EST database sequences. In order to determine the upstream and downstream coding sequences of mouse GFRα-5, 5' and 3' RACE experiments were performed. Since these experiments did not work as expected and since, at some points, frame shifts had to be introduced in the mouse GFRα-5 sequence to yield consistent homology with other GFRα's after translation, we decided to shift to the cloning of the rat homologue of mouse GFRα-5.

Identification and cloning of rat GFRα-5 cDNA sequences

The cDNA sequences with accession number AU035938 and AA823200 described above were used as the query sequence in BLAST searches on the proprietary LifeSeq and ZooSeq databases (Incyte Pharmaceuticals, Palo Alto, CA, USA). Two rat clones with high homology to the mouse GFRα-5 sequences were identified: number 701290919H1 (270 bp; hit with AU035938 (SSP = 1.1e-32) and with AA823200 (SSP = 1.3e-21)) and number 701291473H1 (250 bp; hit only with AA823200 (SSP = 4.3e-42)). From comparing the translated protein sequences derived from clones 701291473H1 and 701290919H1 to the known GFRα protein sequences, it could be deduced that sequence 701290919H1 was probably localised 5′ to sequence 701291473H1 and that these sequences were almost adjacent to each other in the full GFRα-5 cDNA sequence. Therefore, two forward primers (RAT-GFRα5-sp1 and RAT-GFRα5-sp2) were designed in the 5′ region of sequence 701290919H1 and two reverse primers (RAT-GFRα5-ap1 and RAT-GFRα5-ap2) in the 3′ region of sequence 701291473H1. All primer sequences used in PCR experiments are summarized in Table 3.

Table 3: Primers used for the amplification of rat GFRα-5 sequences. The RACE-ap1 and RACE-ap2 primers are included in the Marathon Ready™ cDNA kit.

Name	Sequence	n
RAT-GFRα5-sp1	GTGGTCACCCCCAACTACCTGG	22
RAT-GFRα5-sp2	GCCTTCCGCAAGCTTTTTACAAGG	24
RAT-GFRα5-sp3	GCTCTTCTGCGGATGCGAAGGC	22
RAT-GFRα5-sp4	AGCTGCCGGGTTTACTGATGCTAC	24
RAT-GFRα5-sp5	GATGCTACTCTCCCAAGGTCAGGC	24
RAT-GFRα5-sp6	CTGGTAAGCTTTAAGGCAGAGGAGACC	27
RAT-GFRα5-ap1	CATGGCAGTCAGCTGTGTTGTCC	23
RAT-GFRα5-ap2	CAGCTGTGTTGTCCATGGTTCACC	24
RAT-GFRα5-ap3	TGGTTGCGAGCTGTCAAAGGCTTGTATGGC	30
RAT-GFRα5-ap4	GGGGTTCCTTGTAAAAAGCTTGCGGAAGGC	30
RAT-GFRα5-ap5	GGTCCAAGGGCTTCAGGCAGGAAGG	25
RAT-GFRα5-ap6	GCCTTCGCATCCGCAGAAGAGC	22
RAT-GFRα5-ap7	CCAGGTAGTTGGGGGTGACCACG	23
RAT-GFRα5-ap7b	CCCAGGCATTGCGCCACGTA	20
RAT-GFRα5-ap8	CATTGCGCCACGTACTCGGAGC	22
RAT-GFRα5-ap9	GACCTGAGGGCAAGGGAGTTTCA	23
RAT-GFRα5-ap10	GCAAGGGAGTTTCAGTTCAGTGAGC	25
RACE-ap1	CCATCCTAATACGACTCACTATAGGGC	27
RACE-ap2	ACTCACTATAGGGCTCGAGCGGC	23

A PCR was then performed using primers RAT-GFRα5-sp1 and RAT-GFRα5-ap1 on rat brain Quickclone cDNA (Clontech Laboratories, Palo Alto, CA, USA) to confirm the presence of rat GFRα-5 in brain-derived cDNA. Since the DNA sequence coding for the rat GFRα-5 sequence has a high G+C content in this region, PCR reactions were done using the Advantage-GC PCR kit (Clontech). PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-sp1 and RAT-GFRα5-ap1, 1 µl of Advantage KlenTaq polymerase mix and 1 µl of rat brain

Quickclone cDNA. Samples were heated to 95°C for 1 min and cycling was done for 1 min at 95°C, 1 min at 56°C and 1 min at 72°C for 30 cycles, with a final step of 7 min at 72°C. A nested PCR was then performed on 1 µl of the primary PCR reaction with primers RAT-GFRα5-sp2 and RAT-GFRα5-ap2. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-sp2 and RAT-GFRα5-ap2, 1 µl of Advantage KlenTaq polymerase mix and 1 µl of primary PCR product. Samples were heated to 95°C for 1 min and cycling was done for 30 s at 95°C, 1 min at 56°C and 1 min at 72°C for 25 cycles, with a final step of 7 min at 72°C. PCR products were analysed on a 1% (w/v) agarose gel in 1x TAE buffer (40 mM Tris-acetate, 1 mM EDTA (sodium salt), pH 8.3). Two PCR fragments of approximately 1100 and 200 bp, respectively, were excised from the gel and purified with the Qiaquick gel extraction kit (Qiagen Gmbh, Hilden, Germany). The PCR fragments were sequenced to confirm their identity. The smallest fragment yielded a sequence of 211 bp corresponding to the joined sequences 701290919H1 and 701291473H1. The larger fragment yielded a sequence of 1049 bp of which 18 bp at the 5' end, 59 bp at the 3' end and an internal stretch of 92 bp corresponded to the sequence of the 211 bp fragment, but which had additional sequence stretches in between. This fragment represented a variant of rat GFRα-5.

Both clones 701291919H1 and 701291473H1 were obtained from Incyte Pharmaceuticals and the inserts completely

sequenced. The sequences are included in this application (sequence 3 = 701290919H1 and sequence 4 = 701291473H1). Both clones were derived from the same 7-day old rat brain cortex cDNA library. Both clones differ in their 5' ends (first 134 bp in 701291473H1 and first 227 bp in 701290919H1) but are identical thereafter. Both contain part of the GFRα-5 coding sequence up to a stop codon (position 184-186 in 701291473H1 and 277-279 in 701290919H1). A 3' untranslated region of 549 bp followed by a poly(A)-tail is then present in both clones. We hypothesized that both clones are different variants of the rat GFRα-5 gene. Primers (RAT-GFRα5-ap3 and RAT-GFRα5-ap4) were designed on a part of the sequence common to both variants to perform 5' RACE experiments in order to determine the 5' end of the rat GFRα-5 cDNA.

First, a 5' RACE PCR was performed on rat brain Marathon Ready™ cDNA (Clontech). PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M or 1.5 M GC-MELTä, 200 nM of primers RAT-GFRα5-ap3 and RACE-ap1, 1 µl of Advantage KlenTaq polymerase mix and 5 µl of rat brain Marathon Ready™ cDNA. Samples were heated to 95°C for 30 s and cycling was done for 30 s at 95°C, 4 min at 72°C for 5 cycles, then 30 s at 95°C, 4 min at 70°C for 5 cycles, then 30 s at 95°C, 4 min at 68°C for 25 cycles, with a final step of 7 min at 68°C. A nested PCR was then performed on 1 µl of the primary PCR reaction with primers RAT-GFRα5-ap4 and RACE-ap2. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M or 1.5 M GC-MELTä, 200 nM of

primers RAT-GFRα5-ap4 and RACE-ap2, 1 μl of Advantage KlenTaq polymerase mix and 1 μl of primary PCR product. Cycling was done using exactly the same parameters as for the primary PCR. PCR products were analysed on a 1% (w/v) agarose gel in 1x TAE buffer (40 mM Tris-acetate, 1 mM EDTA (sodium salt), pH 8.3). A fragment of approximately 350 bp was excised from the gel and cloned into the plasmid vector pCR2.1-TOPO using the TOPO TA cloning kit according to manufacturer's instructions (Invitrogen BV, Leek, The Netherlands). One of the resulting clones yielded an insert sequence of 387 bp which extended the rat GFRα-5 sequence in the 5' direction. Upon translation, this additional cDNA sequence yielded a protein sequence without any internal stop codons and with substantial homology to the other known GFRα sequences. Since no putative ATG start codon could be detected within this additional sequence, novel primers (RAT-GFRα5-ap5 and RAT-GFRα5-ap6) were designed at the 5' end of this sequence to perform additional 5' RACE experiments. First, a 5' RACE PCR was performed on rat heart Marathon Ready™ cDNA (Clontech). PCR reactions were performed in a total volume of 50 μl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-ap5 and RACE-ap1, 1 μl of Advantage KlenTaq polymerase mix and 5 μl of rat heart Marathon Ready™ cDNA. Samples were heated to 95°C for 30 s and cycling was done for 30 s at 95°C, 4 min at 72°C for 5 cycles, then 30 s at 95°C, 4 min at 70°C for 5 cycles, then 30 s at 95°C, 4 min at 68°C for 25 cycles, with a final step of 7 min at 68°C. A nested PCR was then performed on 1 μl of the primary PCR

reaction with primers RAT-GFRα5-ap6 and RACE-ap2. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-ap6 and RACE-ap2, 1 µl of Advantage KlenTaq polymerase mix and 1 µl of primary PCR product. Cycling was done using exactly the same parameters as for the primary PCR. PCR products were analysed on a 1% agarose gel. A fragment of approximately 200 bp was excised from the gel and cloned into the plasmid vector pCR2.1-TOPO using the TOPO TA cloning kit as described above.

Sequencing of two resulting clones extended the rat GFRα-5 sequence with another 128 bp in the 5' direction. Based on this sequence, another primer set (RAT-GFRα5-ap7 and RAT-GFRα5-ap8) was designed to perform additional 5' RACE experiments. RACE PCR was performed on rat brain, heart and kidney Marathon Ready™ cDNA. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-ap7b and RACE-ap1, 1 µl of Advantage KlenTaq polymerase mix and 5 µl of rat heart, brain or kidney Marathon Ready™ cDNA. Samples were heated to 95°C for 30 s and cycling was done for 30 s at 95°C, 4 min at 72°C for 5 cycles, then 30 s at 95°C, 4 min at 70°C for 5 cycles, then 30 s at 95°C, 4 min at 68°C for 25 cycles, with a final step of 7 min at 68°C. A nested PCR was then performed on 1 µl of the primary PCR reaction with primers RAT-GFRα5-ap8 and RACE-ap2. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-ap8

and RACE-ap2, 1 μl of Advantage KlenTaq polymerase mix and 1 μl of primary PCR product. Cycling was done using exactly the same parameters as for the primary PCR. PCR products were analysed on a 1% agarose gel. Several fragments ranging in size from approximately 200 bp to 1200 bp were visible on the gel and were excised and cloned in vector pCR2.1-TOPO using TOPO-TA cloning. The inserts of several clones were sequenced. From these clones, the sequence of rat GFRα-5 could be extended in the 5′ direction. Two different sequences were identified. One sequence extended the ratGFRα-5 sequence with 215 bp in the 5′ direction and included an in-frame start codon preceded by an in-frame upstream stop codon. The resulting predicted protein sequence (52 additional amino acid residues) includes a predicted signal peptide of 29 amino acid residues (as determined by the SPScan program included in the Wisconsin package version 10.0, Genetics Computer Group (GCG), Madison, Wisconsin, USA; score 7.0, probability 1.171e-02). The other sequence determined by these 5′ RACE experiments extended the ratGFRα-5 sequence with 552 bp in the 5′ direction and also included an in-frame start codon preceded by an in-frame upstream stop codon. The most 3′ 79 base pairs of this novel sequence were identical to the 3′ 79 base pairs of the 215 bp sequence, but the rest of the sequence was different. The resulting predicted protein sequence (113 additional amino acid residues), however, did not have a predicted signal peptide sequence at the NH_2-terminus (SPScan, GCG package). The different partial cDNA sequences resulting from the subsequent 5′ RACE experiments together with the

sequences from the Incyte database were compared and merged into several possible rat GFRα-5 variants. In order to identify which of the identified variants are real, primers were designed 5' of the translation start codon (primers RAT-GFRα5-sp4 and RAT-GFRα5-sp5 for the "long" 5' variant resulting from the 552 bp RACE fragment and RAT-GFRα5-sp6 for the "short" 5' variant resulting from the 215 bp RACE fragment) and 3' of the translation stop codon (RAT-GFRα5-ap9 and RAT-GFRα5-ap10). These primers were then used to amplify the full GFRα-5 coding sequences using cDNA derived from different rat tissues.

First, sequences coding for the "long" 5' variant were amplified by PCR. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-sp4 and RAT-GFRα5-ap9, 1 µl of Advantage KlenTaq polymerase mix and 5 µl of rat heart, brain or kidney Marathon Ready™ cDNA. Samples were heated to 95°C for 1 min and cycling was done for 45 s at 95°C, 1 min at 57°C and 1 min at 72°C for 35 cycles, with a final step of 7 min at 72°C. A nested PCR was then performed on the primary PCR reaction with primers RAT-GFRα5-sp5 and RAT-GFRα5-ap10. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-sp5 and RAT-GFRα5-ap10, 1 µl of Advantage KlenTaq polymerase mix and 1 µl of primary PCR product. Cycling was done using exactly the same parameters as for the primary PCR, except that 30 PCR cycles were

done instead of 35. PCR products were analysed on a 1% agarose gel. Several fragments ranging in size from approximately 1000 to 1250 bp were excised from gel and cloned in vector pCR2.1-TOPO using TOPO-TA cloning. The inserts of several clones were sequenced. Next, sequences coding for the "short" 5' variant were amplified by PCR. PCR reactions were performed in a total volume of 50 µl, containing 1x GC cDNA PCR reaction buffer, 0.2 mM dNTP, 1 M GC-MELTä, 200 nM of primers RAT-GFRα5-sp6 and RAT-GFRα5-ap9, 1 µl of Advantage KlenTaq polymerase mix and 5 µl of rat heart Marathon Ready™ cDNA. Samples were heated to 95°C for 5 min and cycling was done for 30 s at 94°C, 1 min at 57°C and 2 min 30 s at 72°C for 35 cycles, with a final step of 7 min at 72°C. PCR products were analysed on a 1% agarose gel. Several fragments ranging in size from approximately 1500 to 2200 bp were excised from gel and cloned in vector pCR2.1-TOPO using TOPO-TA cloning. The inserts of several clones were sequenced. Analysis of all the obtained sequences (16 resulting clones were completely sequenced) allowed the rat GFRα-5 DNA sequence to be divided into 6 sequence stretches common to all identified variants, with 5 intervening sequence stretches present or absent depending on the variant. All 5 intervening sequences contain 5' and 3' splice site consensus sites (GT at the 5' end and AG at the 3' end of the intron sequence) (Senapathy et al., 1990) (see table 4 below) and could thus potentially represent unspliced introns.

In order to strengthen the hypothesis that the

identified variants could result from the conservation of unspliced introns in certain mRNA transcripts, the rat GFRα-5 sequence was compared to the genomic sequence of human GFRα-1 (Angrist et al., 1998). From this analysis, it was apparent that the GFRα-5 sequences common to all transcripts coincided with exons in GFRα-1 (see table 4 below). The intervening sequences absent in some transcripts coincided with intron sequences in human GFRα-1. Therefore, we considered all intervening sequences as unspliced introns. The intron present between exon 5 and exon 6 can be spliced out in two different ways and results in the presence of two different splice variants of rat GFRα-5, which we have called variant A and variant B.

Sequence 5 shows the consensus sequence for rat GFRα-5 including the intron sequences (intron 1: bp 125 to 684; intron 2: bp 1040 to 1088; intron 3: bp 1199 to 1278; intron 4: bp 1414 to 2154; intron 5A: bp 2247 to 2385 and intron 5B: bp 2231 to 2314). *A polymorphism was detected at position 2244 in sequence 5, with T found in 50% of the sequenced clones and C in the other 50%. This polymorphism leads to an amino acid change in the protein (variant A) from W to R, in the hydrophobic region involved in GPI-anchoring.*

Figure 1 schematically shows the structure of the rat GFRα-5 gene together with the derived cDNA for splice variants A and B after splicing out of the intron sequences and the translated protein sequences of variants A and B with their characteristics.

Table 4 shows the DNA sequence at the intron-exon

boundaries together with the sizes of identified introns and exons. The right column shows the sizes of the corresponding exons in the genomic sequence of human GFRα-1 (from Angrist et al., 1998).

Table 4: Intron-exon structure of rat GFRα-5.

Exon	Size (bp)	Intron size (bp)	Splice acceptor	Splice donor	Corresponding GFRα-1 exon size (bp)
1	>124	560	---	GAGgtaaggaggt	---
2	355	49	ccctcaccagGGT	CCGgtgcgtgcgg	337
3	110	80	gcgcgcgcagGCC	TAGgtacgctggg	110
4	135	741	gtccctgcagGCA	TGGgtgaggggggc	135
5	92	139 (varA) 84 (varB)	cactccatagATG	CGGgtaggtatgg TGGgtgctgtttc	182
6	>137	---	ttgtcccaagGTG ccctttctcagGCA	–	753

The consensus sequence obtained by removing introns 1 to 4 and intron 5A (sequence 6; variant A) translates into a protein of 273 amino acid residues with a calculated molecular mass of 29.7 kDa and an isoelectric point of 8.92 (sequence 8). The consensus sequence obtained by removing introns 1 to 4 and intron 5B (sequence 7; variant B) translates into a protein of *258* amino acid residues with a calculated molecular mass of *28.0* kDa and an isoelectric point of *8.91* (sequence 9). Figure 2 shows the alignment of variants A and B of rat GFRα-5. The protein sequences are both similar to the known GFRα sequences and only differ from each other in a small amino acid stretch at the carboxy-terminus. These two sequences probably represent biologically active GFRα-5 variants. Since all the other variants sequenced contain one or more intron sequences, they are probably intermediates of

RNA processing. It is not clear why all these intermediates are present in cDNA derived from purified mRNA and why it is so difficult to amplify a cDNA sequence derived from a completely spliced mRNA transcript. GFRα-1 to -4 are characterized by a COOH-terminal sequence typical of a glycosyl-phosphatidyl inositol (GPI)-anchored protein, consisting of a hydrophobic region of 17-31 amino acid residues preceded by a hydrophilic sequence containing a stretch of three small amino acids such as Asp, Cys, Ala, Ser, Gly or Asn (Gerber et al., 1992). The rat GFRα-5 variant A protein sequence has a hydrophobic carboxy-terminus of 21 amino acid residues (position 253 to 273) preceded by two possible GPI cleavage sites (DSS at position 234 to 236 or NAG at position 250-252). *Variant B has a shorter hydrophilic carboxy-terminus, implying that no GPI-anchoring is possible for this variant. This could mean that variant B is a soluble form of the rat GFRα-5 receptor.* A predicted signal peptide of 29 amino acids is present in both variants (as determined by the SPScan program included in the GCG package; score 7.0, probability 1.171e-02). In addition, one possible site for N-linked glycosylation (NVS at position 192 to 194 in the protein) is present.

Recently, a model has been proposed for the domain structure of GFRα's based on the comparison of the sequences of mouse GFRα-1 to -3 and chicken GFRα-4 (Airaksinen et al., 1999). The model includes three conserved cysteine-rich domains joined together by less conserved adaptor sequences. The molecules are

anchored to the membrane by a GPI-anchor. Rat GFRα-5 conforms partly to this model, since it also contains the second and third cysteine-rich region and a possible GPI-anchor *(at least for variant A)*. However, it differs significantly from the other GFRα's in that the first cysteine-rich region is absent.

Figure 3 shows the alignment of rat GFRα-5 variants A and B with rat GFRα-1 (EMBL acc. no. U59486), rat GFRα-2 (EMBL acc. no. AF003825), mouse GFRα-3 (EMBL acc. no. AB008833) and chicken GFRα-4 (EMBL acc. no. AF045162). The alignment was done using the ClustalW alignment program (EMBL, Heidelberg, Germany). The percentage identity and percentage similarity between members of the GFRα family were calculated by pairwise comparison of the sequences using the GeneDoc software tool (version 2.5.000) and the results are presented in Table 5 below.

Table 5: % identity and % similarity (between brackets) between members of the GFRα family. Accession numbers of the sequences used in the analysis are mentioned in the text.

	rGFRα-1	rGFRα-2	mGFRα-3	cGFRα-4	rGFRα-5(A)	rGFRα-5(B)
rGFRα-1	100	43 (60)	15 (23)	38 (55)	20 (29)	20 (28)
rGFRα-2		100	18 (28)	40 (56)	21 (32)	21 (31)
mGFRα-3			100	16 (25)	22 (30)	20 (29)
cGFRα-4				100	27 (37)	26 (35)
rGFRα-5(A)					100	92 (92)
rGFRα-5(B)						100

Four members of the GDNF family of neurotrophic factors have been identified so far (GDNF, NTN, PSP, EVN/ARTN). All four signal through binding to a

specific GPI-linked GFRα receptor (GFRα-1 for GDNF, GFRα-2 for NTN, GFRα-3 for EVN/ARTN and (chicken) GFRα-4 for PSP) in combination with a common transmembrane tyrosine kinase, cRET. GFRα-4, the coreceptor for PSP, has been identified in chicken only and no mammalian counterpart has been found yet.

The similarity between the rat GFRα-5 described in the present application and the chicken GFRα-4 is 37% (27% identity) suggesting that rat GFRα-5 is a novel member of the GFRα family. GFRα-5 could be the mammalian persephin receptor or, alternatively, could be the receptor for an unidentified GDNF family member.

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List of abbreviations

ARTN	artemin
BLAST	basic local alignment search tool
bp	base pairs
cDNA	complementary DNA
CNS	central nervous system
EST	expressed sequence tag
EVN	enovin
GDNF	glial cell-line derived neurotrophic factor
GFRα	GDNF family receptor α
GPI	glycosyl phosphatidyl inositol
NTN	neurturin
PCR	polymerase chain reaction
PNS	peripheral nervous system
PSP	persephin
SSP	smallest sum probability
TGF-β	transforming growth factor β

Sequence Listing

```
   1  GTGCGCCGAG CGCCGGCGCC AGACTTTCGC GCCCGCCTGC GCGTTCTCCG GCCCGGGGTT GGTGCCGCCC TCTTGCCTGG
  81  AGCCCCTGGA GCGCTGCGAG CGCAGCCGCC TGTGCCGGTG CGTGCGTGCG GGGCGGGCTG GGCCGCTCAC CCGCGTCCGG
 161  GCGCGCGCAG GCCCCGTCTC CTTGCCTTCC AGGCCTCATG CGCTCCCGCG CCCGGCTCCC GCGACCGCTG CCCGGAGGAG
 241  GGGGGCCCGC GTTGTCTGCG CGTCTACGCA GGCCTCATGG GCACCGTGGT CACCCCCAAC TACCTGGACA ACGTGAGCGC
 321  GCGCGTTGCG CCCTGGTGCG GCTGTGCGGC CAGTGGAAAC CGGCGCGAAG AATGCGAAGC CTTCCGCAAG CTCTTTACAA
 401  GGAACCCCTG CTTGGGTGAG GGGGCCTGGA GGTCCCGGGG AACCACGGAT GTCTGTGGCC CAATCCAAGC TGCCTGGCCC
 481  GTGGGTCTTA TTTACGTCGC ATCATGTTTG GTGTGGGCGA TGGACAATGT GCACATGCCA TGGTACGTGG GTGGAAGTCA
 561  AGCGTTAAAA CGTGTCCAAT GGNCTGGAAG TTGGCCTTCC TTTTGACACT NATGGGGTGG GCCTTTCTTC ATGGTGNGCC
 641  CAACTTACCT TTGGTTGGTC TTGNCTCTGG GTGGGAATGG CTTNAATTNC AGAATTTTGG GGGTCTTGTT TGAAGCCTGG
 721  CTTTTGGNCT TAANAACTTG ANAAGTTAAA CTCTTATTAA TCCCAATGGG GTTCACCTGT AAAGGGAGAG GG
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Sequence ID No. 1: EMBL acc. no. AU035938 partially coding for mouse GFRα-5.

```
   1  GTGGAACCGG CGCGAAGAAT GCGAACCTTC CGCAAGCTCT TTACAAGGAA CCCCTGCTTG GATGGTGCCA TACAAGCCTT
  81  TGACAGCTTG CAGCCATCAG TTCTGCAGGA CCAGACTGCT GGGTGCTGTT TCCCGCGGGC AAGGCACGAG TGGCCTGAGA
 161  AGAGCTGGAG GCAGAAACAG TCCTTGTTTT GTCCTAACGC CCAAGGTGTC CTGGCTGTAT GCACTCACTG CCCTGGCTCT
 241  CCAGGCCCTG CTCTGATTAG GAACATGAAC CGTGGACGAC ACAGCTGACT GCCATGTCTC CCGATGACTG CTCACTGAGC
 321  TGAAACTCCC TTGCCCTCAG GTCTGCTGCC CTTTGCAGGC CTGGACCCCT GTGTGGCTGT CCTCTGGATT GGGGGCTGGA
 401  GGCTAGGGTC TGACTGAAAA GCCTGTGTTC CCGTCAGTAG GCATCTTGTC CATTTTCTTC CCCATCCTAG AGCTGAGCAC
 481  CCATAGATGA GGCCTCA
```

Sequence ID No. 2: EMBL acc. no. AA823200 partially coding for mouse GFRα-5.

```
   1  GGCACCGTGG TCACCCCCAA CTACCTGGAC AACGTGAGCG CGCGCGTTGC GCCCTGGTGC GGCTGTGAGG CCAGCGGAAA
  81  CCGGCGCGAA GAGTGCGAAG CCTTCCGCAA GCTTTTTACA AGGAACCCCT GCTTGGATGG TGCCATACAA GCCTTTGACA
 161  GCTCGCAACC ATCAGTTCTG CAGGACCAGT GGAACCCCTA CCAGAATGCT GGGTGCTGTT TCCTGTGGGT GTCCTCGATG
 241  TCCATACTCA CTGCCCTGGC TCTCCAGGCC CTGCTCTAAT TAGGAAGGTG AACCATGGAC AACACAGCTG ACTGCCATGT
 321  CTCTGGATTA TGCTCACTGA ACTGAAACTC CCTTGCCCTC AGGTCTGCTG TCCTTTGCAG TTCTGGACCC CTGCATGGCT
 401  GTCTCCTGGA CTGGGAGCTG GAGGCTAGGG CCCGACTGTT AGGTTCCCCT GTTAGTAGGC ATCTCGCCTG TTTTCTTCAC
 481  CATCCTTGAG ATGATGGTAG ATGATATTTA GCACCTGTAG ACAGGGCCTC ATTGGGCCCC TTGGGCTTAC AGAGCAGAAC
 561  AGAGACTAGC CTCCTGCTCT TAGAATTGGG TAGTGTTCTT TTCCAAGAAG ACATGGCACT AAGGCGATCA TATGAACAGA
 641  CTGACAGACT GCAGTCTAAA TACCCATGCC CCAGGGCCAG CGCTGACCTT GCTTGTCACC TATGACATGG CGCTGTGTAG
 721  GGATTAAAGA GAGAGATTCA GGTCCCTCCT GCTGGACATC CCACTGGCCT CCCAGACTCT CCCAGCACCT GCAGTGGCAC
 801  AGCAGCTCAA TAAACCCATG TGCACTGGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 881  AAAAAGAAAA AAAAAAAAAA A
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Sequence ID No. 3: Incyte clone number 701290919H1 partially coding for rat GFRα-5.

```
   1  GTATGGGGAG AGGATGTGGA GTTGGCAGTT TCTCATCGTT CCCTTCTGTA TTTACCCTTC TCAGGCAGGC CAAGGTGGAG
  81  GCCTGAGTGG CCTGAGAAGA GATGGAGGCA GAAACGGTCC CCGTTTTGTC CCAAGGTGTC CTCGATGTCC ATACTCACTG
 161  CCCTGGCTCT CCAGGCCCTG CTCTAATTAG GAAGGTGAAC CATGGACAAC ACAGCTGACT GCCATGTCTC TGGATTATGC
 241  TCACTGAACT GAAACTCCCT TGCCCTCAGG TCTGCTGTCC TTTGCAGTTC TGGACCCCTG CATGGCTGTC TCCTGGACTG
 321  GGAGCTGGAG GCTAGGGCCC GACTGTTAGG TTCCCCTGTT AGTAGGCATC TCGCCTGTTT TCTTCACCAT CCTTGAGATG
 401  ATGGTAGATG ATATTTAGCA CCTGTAGACA GGGCCTCATT GGGCCCCTTG GGCTTACAGA GCAGAACAGA GACTAGCCTC
 481  CTGCTCTTAG AATTGGGTAG TGTTCTTTTC CAAGAAGACA TGGCACTAAG GCGATCATAT GAACAGACTG ACAGACTGCA
 561  GTCTAAATAC CCATGCCCCA GGGCCAGCGC TGACCTTGCT TGTCACCTAT GACATGGCGC TGTGTAGGGA TTAAAGAGAG
 641  AGATTCAGGT CCCTCCTGCT GGACATCCCA CTGGCCTCCC AGACTCTCCC AGCACCTGCA GTGGCACAGC AGCTCAATAA
 721  ACCCATGTGC ACTGGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
 801  AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGAAA AAAAAAAAAA AA
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Sequence ID No. 4: Incyte clone number 701291473H1 partially coding for rat GFRα-5.

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   1  CTGGTAAGCT TTAAGGCAGA GGAGACCTAA GAGCTGAGAC ATGCTATGTT GAGTGGAGCG TATTTACGGG TGCTGAATGA
 161  TTTGGTGACT TGGCTGGATT TGCATATGTC CAGTGCCAAG TTCAGACATA GCTGCCGGGT TTACTGATGC TACTCTCCCA
 241  AGGTCAGGCA TTCTATTTTC CCCTGAATGG CTTTTCATCT GTGACTTATC TACATCTTCA CTGAAACTAC TGGTAAACGT
 321  CCAGGTCTGT CTCAGGGCGA AGTCCTATGG TCTGCCATTA AGCCTCAGTG TCCTGTCAGG TGAAGCTGGG GAGGATGGAA
 401  GGGGTCCAGT AGACGCTCTG TGATGCATGT GCCAGTTCTG GAGATGGTGG TGGAGGCTGA ACCTGAGCTT CTGGGGAACC
 481  TCCGAGTACT GCCTCCATTC ACGACCTGGG TGGATATCCC TAGGACCTGC CCATGCCCGC TTCCTCAGGA AAAACGGGTC
 561  ACGCCTATGG GCCACACTCT CTCCCCTTGG GTTTGGGTAT CTGCCCCCAG CCCCCGCCAA ATTCCGGGGT GTGGAATGTG
 641  GAGAACCAAG CACAGAGGGC TGCAGCCTGC CCTCCCCTCA CCAGGGTCAG CGAGCTCCAC TGAGGGGAAT CGCTGCGTGG
 721  AAGCAGCCGA GGCGTGCACA GCAGACGAGC AGTGCCAGCA GCTGCGCTCC GAGTACGTGG CGCAATGCCT GGGCCGGGCG
 801  GGCTGGCGGG GACCCGGGAG CTGCGTGCGC TCCCGCTGCC GCCGTGCCCT GCGCCGCTTC TTCGCCCGCG GGCCTCCGGC
 881  GCTCACGCAC GCGCTGCTCT TCTGCGGATG CGAAGGCCCC GCGTGCGCCG AGCGCCGGCG CCAGACATTC GCGCCCGCCT
 961  GCGCGTTCTC CGGCCCCCAG CTGGCGCCAC CTTCCTGCCT GAAGCCCTTG GACCGCTGCG AGCGAAGCCG CCGGTGCCGG
1041  TGCGTGCGGG GCGGGCTGGG CCGCTCACCG GCGTCCGGGC GCGCGCAGGC CCCGTCTCTT TGCCTTCCAG GCCTCATGCG
1121  CTCCCGCGCC CGGCTCCCGC GACGGCTGTC CGGAGGAGGG GGGCCCGCGG TGTCTGCGCG CCTACGCAGG CCTTGTAGGT
1201  ACGCTGGGCG GCCTCTGGCG GGCGGGGCGG CGGAGGCAGA TTCCGGGGGC CCGTCACAGG TCCTGGGGGT CCCTGCAGGC
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1361  GCGCGAAGAG TGCGAAGCCT TCCGCAAGCT TTTTACAAGG AACCCCTGCT TGGGTGAGGG GGCTGGAGAG CCCGGGCAAC
1441  CAAGGACGTC TATGGCCCAG TCTAGGCTGC CTGGCCTGTG GGGACCCTTA AAATGTTTTC GTCGTGTCGT ATTTGGTGTG
1521  GGTGATGGAC AGTGTGCACG TGCCATGGTG CATGGGTGGA AGTCAGAGGA CAACTTGTCA GTCTCTTTCT ACCACGTGGG
1601  TCCCCGGGAT AGCACTGGGC TCATCAGTTT TGGTGGCAAG TGCCTTTGCC TGCTGAGCCA TCTTGCTGGC TGATGTGAGC
1681  ACATTTTTGA TGGAAAGAAA CTGAGGTTTC CAGAGACCAG ATAGCCGATC ACTAGAGAAT TCGAGAGATG TCAAGAATCT
1761  CTTAGGGCTA GAAAGGATGA GTTAAAACAT GTCCAATGAC CTGGAGTTGG CCAAGGCTCC CTTTGGCACT ACTGAGGTCT
1841  TTTCCTCCAT GTGTTCCCAA TTTAACGCTG CTGTTCTTGC CTCGGGATGA AATAGCGTTG TTCCAGATTT CTGGGGGCCC
1921  GGTTTGAAGC CTGTCTCTGC CACTTCGTAG CCGAGAGTTA AACTCTTATT AATCCTAATT GTGTTCACCT GTAAGGGCGG
2001  GGTGTGCACT TGTCAACCTC ACTCTTAGCA CAGTGACCTT CCATCTCAGG CCGTGCCTTG CAGATTCCAG GGGGTGTCTC
2081  ATTTTGTCTC AAGGGAGTGG AGCTGTTTCT AGGGTTTCCT GGCCAAACCT TCTCTGGATC TCTCCACTCC ATAGATGGTG
2161  CCATACAAGC CTTTGACAGC TCGCAACCAT CAGTTCTGCA GGACCAGTGG AACCCCTACC AGAATGCTGG GTGCTGTTTC
2241  CTGTGGGTAG GTATGGGGAG AGGATGTGGA GTTGGCAGTT TCTCATCGTT CCCTTCTGTA TTTACCCTTC TCAGGCAGGC
2321  CAAGGTGGAG GCCTGAGTGG CCTGAGAAGA GATGGAGGCA GAAACGGTCC CCGTTTTGTC CCAAGGTGTC CTCGATGTCC
2401  ATACTCACTG CCCTGGCTCT CCAGGCCCTG CTCTAATTAG GAAGGTGAAC CATGGACAAC ACAGCTGACT GCCATGTCTC
2481  TGGATTATGC TCACTGAACT GAAACTCCCT TGCCCTCAGG TC
```

Sequence ID No. 5: Consensus sequence for the rat GFRα-5 gene including the exon and intron sequences. At position 2244, a C is present instead of a T in 50% of the sequenced clones.

```
   1  CTGGTAAGCT TTAAGGCAGA GGAGACCTAA GAGCTGAGAC ATGCTATGTT GAGTGGAGCG TATTTACGGG TGCTGAATGA
  81  GAGGCCAGGC CAGGCAGTTT TATGGAGTCT TGGATGCCAG AGAGGGTCAG CGAGCTCCAC TGAGGGGAAT CGCTGCGTGG
 161  AAGCAGCCGA GGCGTGCACA GCAGACGAGC AGTGCCAGCA GCTGCGCTCC GAGTACGTGG CGCAATGCCT GGGCCGGGCG
 241  GGCTGGCGGG GACCCGGGAG CTGCGTGCGC TCCCGCTGCC GCCGTGCCCT GCGCCGCTTC TTCGCCCGCG GGCCTCCGGC
 321  GCTCACGCAC GCGCTGCTCT TCTGCGGATG CGAAGGCCCC GCGTGCGCCG AGCGCCGGCG CCAGACATTC GCGCCCGCCT
 401  GCGCGTTCTC CGGCCCCCAG CTGGCGCCAC CTTCCTGCCT GAAGCCCTTG GACCGCTGCG AGCGAAGCCG CCGGTGCCGG
 481  CCCCGTCTCT TTGCCTTCCA GGCCTCATGC GCTCCCGCGC CCGGCTCCCG CGACGGCTGT CCGGAGGAGG GGGGCCCGCG
 561  GTGTCTGCGC GCCTACGCAG GCCTTGTAGG CACCGTGGTC ACCCCCAACT ACCTGGACAA CGTGAGCGCG CGCGTTGCGC
 641  CCTGGTGCGG CTGTGAGGCC AGCGGAAACC GGCGCGAAGA GTGCGAAGCC TTCCGCAAGC TTTTTACAAG GAACCCCTGC
 721  TTGGATGGTG CCATACAAGC CTTTGACAGC TCGCAACCAT CAGTTCTGCA GGACCAGTGG AACCCCTACC AGAATGCTGG
 801  GTGCTGTTTC CTGTGGGTGT CCTCGATGTC CATACTCACT GCCCTGGCTC TCCAGGCCCT GCTCTAATTA GGAAGGTGAA
 881  CCATGGACAA CACAGCTGAC TGCCATGTCT CTGGATTATG CTCACTGAAC TGAAACTCCC TTGCCCTCAG GTC
```

Sequence ID No. 6: Consensus sequence for the rat GFRα-5 cDNA (splice variant A). At position 814, a C is present instead of a T in 50% of the sequenced clones.

```
   1  CTGGTAAGCT TTAAGGCAGA GGAGACCTAA GAGCTGAGAC ATGCTATGTT GAGTGGAGCG TATTTACGGG TGCTGAATGA
  81  GAGGCCAGGC CAGGCAGTTT TATGGAGTCT TGGATGCCAG AGAGGGTCAG CGAGCTCCAC TGAGGGGAAT CGCTGCGTGG
 161  AAGCAGCCGA GGCGTGCACA GCAGACGAGC AGTGCCAGCA GCTGCGCTCC GAGTACGTGG CGCAATGCCT GGGCCGGGCG
 241  GGCTGGCGGG GACCCGGGAG CTGCGTGCGC TCCCGCTGCC GCCGTGCCCT GCGCCGCTTC TTCGCCCGCG GGCCTCCGGC
 321  GCTCACGCAC GCGCTGCTCT TCTGCGGATG CGAAGGCCCC GCGTGCGCCG AGCGCCGGCG CCAGACATTC GCGCCCGCCT
 401  GCGCGTTCTC CGGCCCCCAG CTGGCGCCAC CTTCCTGCCT GAAGCCCTTG GACCGCTGCG AGCGAAGCCG CCGGTGCCGG
 481  CCCCGTCTCT TTGCCTTCCA GGCCTCATGC GCTCCCGCGC CCGGCTCCCG CGACGGCTGT CCGGAGGAGG GGGGCCCGCG
 561  GTGTCTGCGC GCCTACGCAG GCCTTGTAGG CACCGTGGTC ACCCCCAACT ACCTGGACAA CGTGAGCGCG CGCGTTGCGC
 641  CCTGGTGCGG CTGTGAGGCC AGCGGAAACC GGCGCGAAGA GTGCGAAGCC TTCCGCAAGC TTTTTACAAG GAACCCCTGC
 721  TTGGATGGTG CCATACAAGC CTTTGACAGC TCGCAACCAT CAGTTCTGCA GGACCAGTGG AACCCCTACC AGAATGCTGG
 801  GCAGGCCAAG GTGGAGGCCT GAGTGGCCTG AGAAGAGATG GAGGCAGAAA CGGTCCCCGT TTTGTCCCAA GGTGTCCTCG
 881  ATGTCCATAC TCACTGCCCT GGCTCTCCAG GCCCTGCTCT AATTAGGAAG GTGAACCATG GACAACACAG CTGACTGCCA
 961  TGTCTCTGGA TTATGCTCAC TGAACTGAAA CTCCCTTGCC CTCAGGTC
```

Sequence ID No. 7: Consensus sequence for the rat GFRα-5 cDNA (splice variant B).

```
  1  MLSGAYLRVL NERPGQAVLW SLGCQRGSAS STEGNRCVEA AEACTADEQC
 51  QQLRSEYVAQ CLGRAGWRGP GSCVRSRCRR ALRRFFARGP PALTHALLFC
101  GCEGPACAER RRQTFAPACA FSGPQLAPPS CLKPLDRCER SRRCRPRLFA
151  FQASCAPAPG SRDGCPEEGG PRCLRAYAGL VGTVVTPNYL DNVSARVAPW
201  CGCEASGNRR EECEAFRKLF TRNPCLDGAI QAFDSSQPSV LQDQWNPYQN
251  AGCCFLWVSS MSILTALALQ ALL
```

Sequence ID No. 8: Predicted protein sequence for rat GFRα-5 (splice variant A). Due to a C/T polymorphism in the DNA sequence, the W at position 257 is a R in 50% of the found clones.

```
  1  MLSGAYLRVL NERPGQAVLW SLGCQRGSAS STEGNRCVEA AEACTADEQC
 51  QQLRSEYVAQ CLGRAGWRGP GSCVRSRCRR ALRRFFARGP PALTHALLFC
101  GCEGPACAER RRQTFAPACA FSGPQLAPPS CLKPLDRCER SRRCRPRLFA
151  FQASCAPAPG SRDGCPEEGG PRCLRAYAGL VGTVVTPNYL DNVSARVAPW
201  CGCEASGNRR EECEAFRKLF TRNPCLDGAI QAFDSSQPSV LQDQWNPYQN
251  AGQAKVEA
```

Sequence ID No. 9: Predicted protein sequence for rat GFRα-5 (splice variant B).

Claims

1. A nucleic acid molecule encoding a rat receptor protein designated (GFRα-5) having the amino acid sequence illustrated in Sequence ID No. 8 or 9 or encoding a functional equivalent or bioprecursor of said receptor.

2. A nucleic acid molecule according to claim 1 which is a DNA molecule.

3. A nucleic acid molecule according to claim 2, wherein said DNA molecule is a cDNA molecule.

4. A nucleic acid molecule according to any preceding claim having the sequence illustrated in any of SEQ ID Nos 5,6, or 7 or the complementary sequence thereof.

5. A nucleic acid molecule capable of hybridising to the molecule of any of claims 1 to 4 or the complementary sequences thereof under conditions of high stringency.

6. A GFRα-5 receptor encoded by a nucleic acid molecule according to any of claims 1 to 4.

7. A DNA expression vector comprising a nucleic acid molecule according to any of claims 2 to 4.

8. A host cell transformed or transfected with the vector according to claim 7.

9. A host cell according to claim 8, which cell is a eukaryotic cell.

10. A host cell according to claim 8 or 9 wherein said cell is a mammalian cell.

~~11. A host cell according to claim 10 which cell~~ is a human embryonic kidney cell HEK293 or a Cos-7 cell.

12. A transgenic cell, tissue or organism comprising a transgene capable of expressing a GFRα-5 receptor protein having the amino acid sequence illustrated in Sequence ID No's. 8 or 9 or the amino acid sequence of a functional equivalent or bioprecursor thereof.

13. A transgenic cell tissue or organism according to claim 12, wherein said transgene comprises a nucleic acid molecule according to any of claims 1 to 4.

14. A GFRα-5 receptor protein or a functional equivalent derivative or bioprecursor thereof, expressed by the cell according to any of claims 8 to 13.

15. A HEK293 or Cos-7 cell line trasfected or transformed with the expression vector of claim 7.

16. An antisense molecule comprising a nucleic acid which is capable of hybridising to the nucleic

acid according to any of claims 1 to 4.

17. A molecule according to claim 16 for use as a medicament.

18. Use of a molecule according to claim 16 in the manufacture of a medicament for treating pain or carcinoma.

19. An isolated receptor having the amino acid sequence as illustrated in any of SEQUENCE ID No 8 or 9 or the amino acid sequence of a functional equivalent or bioprecursor of said receptor.

20. A pharmaceutical composition comprising a nucleic acid molecule according to any of claims 1 to 4 together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

21. A pharmaceutical composition comprising a molecule according to claim 16 or a receptor according to claim 19 together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

22. A compound which acts as an agonist or an antagonist in relation to the receptor of claim 19.

23. A pharmaceutical composition comprising an agonist or an antagonist according to claim 22 together with a pharmaceutically acceptable carrier, diluent, or excipient therefor.

24. A method of determining whether a compound is an agonist or an antagonist in relation to a receptor GFRα-5 according to any of claims 6 or 19, which method comprises contacting a cell expressing said receptor with said compound to be tested and monitoring the level of any GFRα5 mediated functional or biological response.

25. A method according to claim 24 wherein said cell is a cell according to any of claims 8 to 13.

26. A method according to claim 24 or 25 wherein the GFRα-5 mediated functional or biological response comprises the level of phosphorylation in said cell.

27. A method of determining whether a compound is an agonist, antagonist or a ligand in relation to GFRα-5 receptor, according to claims 6 or 9, which method comprises contacting a membrane preparation of cells expressing said GFRα-5 with said compound in the presence of cRET or similar protein which interacts with GFRα-5 in the signal transduction pathway of which GFRα5 is a component and monitoring the level of any interaction of GFRα-5 with cRET or said similar protein.

28. A compound identifiable as an agonist by the method according to any of claims 24 to 27 for use as a medicament.

29. Use of a compound identifiable as an agonist by the method according to any of claims 24 to 27 in

the preparation of a medicament for the treatment of neurodegenerative diseases, Alzheimers disease, Parkinsons disease, Motor Neuron Disease, peripheral neuropathy, spinal cord injury, familial hirschsprung disease, carcinomas and diseases associated with GFRα5 receptor dysfunction.

30. A compound identifiable as an antagonist by the method according to any of claims 24 to 27 for use as a medicament.

31. Use of a compound identifiable as an antagonist by the method according to any of claims 24 to 27 in the preparation of a medicament for the treatment of carcinomas or in alleviating pain.

32. A pharmaceutical composition comprising a compound according to claim 28 or 30 together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

33. An antibody specific for GFRα-5 receptor protein having an amino acid sequence as illustrated in Sequence ID No's. 8 or 9 or an amino acid sequence of a functional equivalent or bioprecursor of said receptor.

34. A pharmaceutical composition comprising an antibody according to claim 33 together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

35. A method of identifying ligands for GFRα-5 receptor protein, which method comprises contacting a receptor according to claim 6 or 9 with a cell extract or a compound to be tested and isolating any molecules bound to said receptor.

36. A method of determining whether a compound is a ligand for GFRα-5 receptor, which method comprises contacting a cell expressing said receptor according to any of claims 8 to 13 with said compound and monitoring the level of any GFRα-5 mediated functional or biological response.

37. A method according to claim 36 which comprises monitoring the level of phosphorylation in said cell.

38. A compound identifiable as a ligand for GFRα-5 according to the method of claims 36 or 37 for use as a medicament.

39. Use of a compound identifiable according to the method of claims 36 or 37 in the preparation of a medicament for the treatment of neurodegenerative diseases, Alzheimers disease, Parkinsons disease, Motor Neuron Disease, peripheral neuropathy, spinal cord injury, familial hirschsprung disease in addition to carcinoma and diseases associated with GFRα5 dysfunction.

40. A kit for determining whether a compound is an agonist or an antagonist of GFRα-5 receptor protein

which kit comprises a cell according to any of claims 8 to 13, means for contacting said cell with said compound and means for monitoring the level of GFRα-5 mediated functional or biological response in said cell.

41. A kit according to claim 40, wherein said GFRα-5 mediated functional or biological response comprises the level of phosphorylation in said cell.

42. A diagnostic kit including a probe which comprises any of, a nucleic acid molecule according to any of claims 1 to 4 or a fragment thereof or an antisense molecule according to claim 16 and means for contacting biological material to be tested with said probe.

43. A kit for determining whether a compound is a ligand of GFRα-5 receptor protein, which kit comprises a membrane preparation from cells expressing GFRα-5, means for contacting said preparation with said compound in the presence of cRET or a similar protein involved in the signal transduction pathway of which GFRα-5 is a component and means for measuring any interaction between GFRα-5 and cRET or said similar protein.